=> d his

(FILE 'HOME' ENTERED AT 14:00:16 ON 07 JUL 2005)

FILE 'REGISTRY' ENTERED AT 14:00:26 ON 07 JUL 2005
        E ACYL CARRIER PROTEIN SYNTHASE/CN
L1   1 S E3

FILE 'CAPLUS' ENTERED AT 14:01:00 ON 07 JUL 2005
L2   378 S L1 OR ACPS OR DPJ OR YDCB
L3   88 S L2 AND (CRYSTAL OR STRUCTURE OR X-RAY OR NMR)
L4   12 S L3 AND SUBTILIS
L5   37 S L3 AND PD<2001
L7   43 S L3 AND (CRYSTAL OR X-RAY OR NMR)
L8   13 S L7 AND PD<2001

=> d his

(FILE 'HOME' ENTERED AT 15:51:49 ON 07 JUL 2005)

FILE 'REGISTRY' ENTERED AT 15:52:11 ON 07 JUL 2005
        E ACYL CARRIER PROTEIN/CN

FILE 'CAPLUS' ENTERED AT 15:52:26 ON 07 JUL 2005
L1   4891 S ACYL CARRIER PROTEIN OR ACP
L2   37 S L1 (S) SUBTILIS
L3   15 S L2 AND PY<2001

WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Thursday, July 07, 2005

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR	
☐	L9	L8 same subtilis	8
☐	L8	(($6acyl adj carrier adj protein adj synth$6) or (holo$ACP adj synth$6) or acps or dpj or ydcb) same (crystal or NMR)	299
☐	L7	($6acyl adj carrier adj protein adj synth$6) or (holo$ACP adj synth$6) or acps or dpj or ydcb	5998

END OF SEARCH HISTORY

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OM protein - protein search, using sw model

Run on: May 20, 2005, 02:26:43 ; Search time 135.522 Seconds
                                        (without alignments)
                                        453.427 Million cell updates/sec

Title: US-10-717-138-2
Perfect score: 595
Sequence: 1 AYGIGLDITELKRIASMAGR..........SITHTKEYAAAQVVIERLSS 120

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_03:*
                1: uniprot_sprot:*
                2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	591	99.3	121	1	ACPS_BACSU *5·30·00*	P96618 bacillus su *Kasahara*
2	313	52.6	119	2	Q81IT7 *6·1·03*	Q81it7 bacillus ce *reus*
3	304	51.1	119	2	Q81JG3 *11*	Q81jg3 bacillus an*thracis*
4	304	51.1	119	2	Q6HPE3 *04*	Q6hpe3 bacillus thu*ngiensis*
5	303	50.9	119	2	Q73ET8 *11*	Q73et8 bacillus ce
6	300	50.4	119	2	Q63GX2	Q63gx2 bacillus ce
7	297	49.9	119	1	ACPS_BACHD	Q9kfg1 bacillus ha
8	287	48.2	118	1	ACPS_LISMO	Q8y812 listeria mo
9	287	48.2	118	2	Q721T0	Q721t0 listeria mo
10	283	47.6	118	1	ACPS_LISIN	Q92dd0 listeria in
11	279.5	47.0	117	1	ACPS_STAEP	Q8cnk6 staphylococ
12	278	46.7	119	1	ACPS_STAAU	Q9zah6 staphylococ
13	277.5	46.6	119	1	ACPS_OCEIH	Q8esk9 oceanobacil
14	275	46.2	119	1	ACPS_STAAM	P63468 staphylococ
15	275	46.2	119	1	ACPS_STAAN	P63469 staphylococ

16	275	46.2	119	1	ACPS_STAAW	P63470	staphylococ
17	275	46.2	119	2	Q6G7N8	Q6g7n8	staphylococ
18	275	46.2	119	2	Q6GF02	Q6gf02	staphylococ
19	269	45.2	117	2	Q820V0	Q820v0	enterococcu
20	261	43.9	119	1	ACPS_LACLA	Q9ch95	lactococcus
21	252.5	42.4	120	1	ACPS_LACPL	Q88z44	lactobacill
22	246.5	41.4	119	2	Q74LB3	Q74lb3	lactobacill
23	245	41.2	117	1	ACPS_LACRE	Q9fcv3	lactobacill
24	243	40.8	120	1	ACPS_STRPN	Q9f7t5	streptococc
25	237.5	39.9	126	1	ACPS_VIBCH	Q9kpb6	vibrio chol
26	233.5	39.2	126	1	ACPS_VIBVU	Q8dc72	vibrio vuln
27	231.5	38.9	126	2	Q7MHP2	Q7mhp2	vibrio vuln
28	228.5	38.4	119	1	ACPS_STRA3	P63471	streptococc
29	228.5	38.4	119	1	ACPS_STRA5	P63472	streptococc
30	227	38.2	119	1	ACPS_STRMU	Q8dsf3	streptococc
31	223.5	37.6	126	1	ACPS_VIBPA	Q87lp3	vibrio para
32	221.5	37.2	124	1	ACPS_CLOAB	Q97lr5	clostridium
33	221	37.1	118	1	ACPS_STRP3	P63473	streptococc
34	221	37.1	118	1	ACPS_STRP8	P63474	streptococc
35	221	37.1	118	1	ACPS_STRPY	Q99y97	streptococc
36	215.5	36.2	133	1	ACPS_CLOPE	Q8xnp1	clostridium
37	213.5	35.9	125	2	Q7VRR2	Q7vrr2	candidatus
38	213.5	35.9	127	1	ACPS_SHEON	Q8eh77	shewanella
39	212	35.6	139	1	ACPS_WIGBR	Q8d303	wiggleswort
40	211.5	35.5	126	2	Q6LMS5	Q6lms5	photobacter
41	206	34.6	122	2	Q6MAG4	Q6mag4	parachlamyd
42	205.5	34.5	125	2	Q67K77	Q67k77	symbiobacte
43	203.5	34.2	126	2	Q7N1X9	Q7n1x9	photorhabdu
44	201.5	33.9	169	1	ACPS_THEMA	Q9wzf6	thermotoga
45	201	33.8	126	1	ACPS_RICPR	Q9zcx5	rickettsia

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OM protein - protein search, using sw model

Run on: May 20, 2005, 02:25:38 ; Search time 78.806 Seconds
                                          (without alignments)
                                          588.931 Million cell updates/sec

Title: US-10-717-138-2
Perfect score: 595
Sequence: 1 AYGIGLDITELKRIASMAGR..........SITHTKEYAAAQVVIERLSS 120

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   595   100.0   120   5   AAU10694 2/02 App1   Aau10694 B. subtil
     2   591   99.3   121   3   AAY88389 7/25/00   Aay88389 B-ydcB es
     3   591   99.3   121   4   AAM52130 2/02 App1   Aam52130 Bacillus
     4   304   51.1   119   6   ABU18305 02   Abu18305 Protein e
     5   287   48.2   118   5   ABB47581 1   Abb47581 Listeria
     6   287   48.2   118   6   ABU32572 //   Abu32572 Protein e
     7   281.5   47.3   124   5   ABP39429   Abp39429 Staphyloc
     8   281.5   47.3   124   8   ADS04560   Ads04560 Staphyloc
     9   279.5   47.0   117   6   ABU42933   Abu42933 Protein e

10	278.5	46.8	119	6	ABU43645	Abu43645	Protein e
11	278	46.7	119	6	ABR83238	Abr83238	S. aureus
12	278	46.7	119	6	ABM71799	Abm71799	Staphyloc
13	277	46.6	119	4	AAU33845	Aau33845	Staphyloc
14	277	46.6	119	4	AAU36808	Aau36808	Staphyloc
15	275	46.2	119	3	AAB14979	Aab14979	Staphyloc
16	275	46.2	119	6	ABU16272	Abu16272	Protein e
17	274	46.1	119	6	ABR83239	Abr83239	S. aureus
18	269	45.2	117	6	ABU29452	Abu29452	Protein e
19	269	45.2	117	8	ADH97041	Adh97041	E. faecal
20	269	45.2	117	8	ADH97039	Adh97039	E. faecal
21	267	44.9	117	4	AAU35183	Aau35183	Enterococ
22	262	44.0	126	6	ABU24470	Abu24470	Protein e
23	261	43.9	119	5	ABB54157	Abb54157	Lactococc
24	260	43.7	129	7	ADC97363	Adc97363	E. faeciu
25	250	42.0	117	6	ADB06134	Adb06134	Alloiococ
26	250	42.0	117	8	ADJ27057	Adj27057	Alloiococ
27	244	41.0	113	6	ADB06132	Adb06132	Alloiococ
28	243	40.8	120	3	AAY58607	Aay58607	Streptoco
29	243	40.8	120	6	ABU02175	Abu02175	S. pneumo
30	243	40.8	120	6	ABU46200	Abu46200	Protein e
31	243	40.8	120	8	ADK46642	Adk46642	Streptoco
32	243	40.8	122	2	AAW80612	Aaw80612	S. pneumo
33	243	40.8	122	4	AAU37879	Aau37879	Streptoco
34	243	40.8	122	4	AAU38056	Aau38056	Streptoco
35	243	40.8	122	7	ADB37480	Adb37480	S. pneumo
36	243	40.8	123	6	ABR83307	Abr83307	S. pneumo
37	243	40.8	123	6	ABR83308	Abr83308	S. pneumo
38	243	40.8	156	3	AAY88388	Aay88388	S-ydcB es
39	243	40.8	157	8	ADR95564	Adr95564	Novel S.
40	237.5	39.9	126	6	ABU49557	Abu49557	Protein e
41	228.5	38.4	119	3	AAY91289	Aay91289	Group B S
42	228.5	38.4	119	5	ABP27225	Abp27225	Streptoco
43	227	38.2	119	6	ABU44498	Abu44498	Protein e
44	221.5	37.2	124	6	ABU23706	Abu23706	Protein e
45	221	37.1	118	5	ABP27226	Abp27226	Streptoco

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OM protein - protein search, using sw model

Run on: May 20, 2005, 02:29:24 ; Search time 21.4925 Seconds
                                         (without alignments)
                                         416.791 Million cell updates/sec

Title: US-10-717-138-2
Perfect score: 595
Sequence: 1 AYGIGLDITELKRIASMAGR..........SITHTKEYAAAQVVIERLSS 120

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score   Match Length DB ID   Description
----
     1   595   100.0   120   4 US-09-770-834-2 *Appl*   . Sequence 2, Appli
  → 2   591   99.3   121   4 US-09-163-446-4 *PD 9198*   Sequence 4, Appli
     3   591   99.3   121   4 US-09-770-834-12 *Appl*   Sequence 12, Appl
     4   281.5   47.3 124   3 US-09-134-001C-4274 *PD98*   Sequence 4274, Ap *Staph*
     5   278   46.7 119   4 US-09-770-834-6 *Appl*   Sequence 6, Appli
     6   260   43.7 129   4 US-09-107-532A-6990   Sequence 6990, Ap
     7   243   40.8 120   4 US-09-583-110-3157   Sequence 3157, Ap
     8   243   40.8 122   3 US-08-987-144-2   Sequence 2, Appli
     9   243   40.8 156   4 US-09-163-446-2   Sequence 2, Appli
    10   243   40.8 157   4 US-09-107-433-4199   Sequence 4199, Ap
    11   209.5   35.2 138   4 US-09-543-681A-7596   Sequence 7596, Ap

12	201.5	33.9	169	4	US-09-770-834-7	Sequence 7, Appli
13	201	33.8	126	4	US-09-770-834-9	Sequence 9, Appli
14	189.5	31.8	126	4	US-08-728-742A-10	Sequence 10, Appl
15	189.5	31.8	126	4	US-09-770-834-8	Sequence 8, Appli
16	189.5	31.8	159	4	US-09-489-039A-11671	Sequence 11671, A
17	177.5	29.8	122	4	US-09-198-452A-330	Sequence 330, App
18	177.5	29.8	122	4	US-09-770-834-4	Sequence 4, Appli
19	177.5	29.8	133	4	US-09-438-185A-315	Sequence 315, App
20	173	29.1	125	4	US-09-770-834-11	Sequence 11, Appl
21	166.5	28.0	119	4	US-09-770-834-5	Sequence 5, Appli
22	152.5	25.6	124	4	US-09-543-681A-6834	Sequence 6834, Ap
23	151	25.4	123	4	US-09-770-834-10	Sequence 10, Appl
24	141.5	23.8	139	4	US-09-770-834-13	Sequence 13, Appl
25	134	22.5	126	4	US-09-902-540-10894	Sequence 10894, A
26	129.5	21.8	122	4	US-09-770-834-3	Sequence 3, Appli
27	124	20.8	121	4	US-08-728-742A-3	Sequence 3, Appli
28	115	19.3	130	4	US-09-770-834-14	Sequence 14, Appl
29	113	19.0	120	4	US-08-728-742A-1	Sequence 1, Appli
30	113	19.0	376	4	US-09-248-796A-17862	Sequence 17862, A
31	107	18.0	131	4	US-09-602-787A-152	Sequence 152, App
32	101	17.0	122	4	US-08-728-742A-4	Sequence 4, Appli
33	91	15.3	119	4	US-08-728-742A-11	Sequence 11, Appl
34	91	15.3	121	4	US-08-728-742A-2	Sequence 2, Appli
35	85.5	14.4	523	4	US-09-252-991A-31596	Sequence 31596, A
36	75.5	12.7	252	4	US-09-543-681A-5523	Sequence 5523, Ap
37	71	11.9	130	4	US-08-728-742A-8	Sequence 8, Appli
38	71	11.9	255	4	US-09-252-991A-19444	Sequence 19444, A
39	69	11.6	168	1	US-08-441-139-10	Sequence 10, Appl
40	69	11.6	187	6	5196523-13	Patent No. 5196523
41	69	11.6	187	6	5196523-13	Patent No. 5196523
42	69	11.6	199	4	US-09-581-001B-7	Sequence 7, Appli
43	69	11.6	253	4	US-09-581-001B-8	Sequence 8, Appli
44	69	11.6	654	1	US-08-441-139-11	Sequence 11, Appl
45	69	11.6	654	4	US-09-919-172-54	Sequence 54, Appl

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OM protein - protein search, using sw model

Run on: May 20, 2005, 02:31:44 ; Search time 105.672 Seconds
                                          (without alignments)
                                          379.865 Million cell updates/sec

Title: US-10-717-138-2
Perfect score: 595
Sequence: 1 AYGIGLDITELKRIASMAGR..........SITHTKEYAAAQVVIERLSS 120

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA:*
          1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
          2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
          3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
          4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
          5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
          6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
          7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
          8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
          9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
         10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
         11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
         12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
         13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
         14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
         15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
         16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
         17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
         18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
         19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
         20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES
          %

Result No.	Score	Query Match	Length	DB	ID	Description
1	595	100.0	120	10	US-09-770-834-2 *Appl*	Sequence 2, Appli
2	595	100.0	120	15	US-10-717-138-2 *Appl*	Sequence 2, Appli
3	591	99.3	121	9	US-09-771-383-1 *PD 1/00*	Sequence 1, Appli *Xtal*
4	591	99.3	121	9	US-09-771-383-11 *"*	Sequence 11, Appl
5	591	99.3	121	10	US-09-770-834-12 *Appl*	Sequence 12, Appl
6	591	99.3	121	15	US-10-717-138-12 *"*	Sequence 12, Appl
7	304	51.1	119	15	US-10-282-122A-46229	Sequence 46229, A
8	287	48.2	118	15	US-10-282-122A-60496	Sequence 60496, A
9	279.5	47.0	117	15	US-10-282-122A-70857	Sequence 70857, A
10	278.5	46.8	119	15	US-10-282-122A-71569	Sequence 71569, A
11	278	46.7	119	9	US-09-771-383-5	Sequence 5, Appli
12	278	46.7	119	10	US-09-770-834-6	Sequence 6, Appli
13	278	46.7	119	15	US-10-717-138-6	Sequence 6, Appli
14	277	46.6	119	9	US-09-815-242-5341	Sequence 5341, Ap
15	277	46.6	119	9	US-09-815-242-12401	Sequence 12401, A
16	275	46.2	119	15	US-10-282-122A-44196	Sequence 44196, A
17	275	46.2	119	17	US-10-857-625-722	Sequence 722, App
18	269	45.2	117	15	US-10-282-122A-57376	Sequence 57376, A
19	267	44.9	117	9	US-09-815-242-10776	Sequence 10776, A
20	262	44.0	126	15	US-10-282-122A-52394	Sequence 52394, A
21	243	40.8	120	15	US-10-282-122A-74124	Sequence 74124, A
22	243	40.8	120	17	US-10-472-928-3504	Sequence 3504, Ap
23	243	40.8	122	9	US-09-815-242-13472	Sequence 13472, A
24	243	40.8	122	9	US-09-815-242-13649	Sequence 13649, A
25	243	40.8	122	10	US-09-897-645-1	Sequence 1, Appli
26	237.5	39.9	126	15	US-10-282-122A-77481	Sequence 77481, A
27	228.5	38.4	119	10	US-09-769-736-30	Sequence 30, Appl
28	227	38.2	119	15	US-10-282-122A-72422	Sequence 72422, A
29	221.5	37.2	124	15	US-10-282-122A-51630	Sequence 51630, A
30	221	37.1	118	15	US-10-282-122A-74722	Sequence 74722, A
31	219.5	36.9	126	15	US-10-282-122A-53036	Sequence 53036, A
32	209.5	35.2	126	15	US-10-282-122A-69169	Sequence 69169, A
33	201.5	33.9	169	9	US-09-771-383-6	Sequence 6, Appli
34	201.5	33.9	169	10	US-09-770-834-7	Sequence 7, Appli
35	201.5	33.9	169	15	US-10-717-138-7	Sequence 7, Appli
36	201	33.8	126	9	US-09-771-383-8	Sequence 8, Appli
37	201	33.8	126	10	US-09-770-834-9	Sequence 9, Appli
38	201	33.8	126	15	US-10-717-138-9	Sequence 9, Appli
39	200.5	33.7	126	15	US-10-282-122A-78498	Sequence 78498, A
40	192.5	32.4	126	9	US-09-815-242-13796	Sequence 13796, A
41	192.5	32.4	126	15	US-10-282-122A-73373	Sequence 73373, A
42	192.5	32.4	126	15	US-10-282-122A-75802	Sequence 75802, A
43	189.5	31.8	126	9	US-09-815-242-10256	Sequence 10256, A
44	189.5	31.8	126	9	US-09-771-383-7	Sequence 7, Appli
45	189.5	31.8	126	10	US-09-770-834-8	Sequence 8, Appli

(handwritten annotation at left: "5DN (not 7) not complex w/ACP")

```
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OM protein - protein search, using sw model

Run on:            May 20, 2005, 02:27:29 ; Search time 14.9254 Seconds
                                            (without alignments)
                                            773.583 Million cell updates/sec

Title:             US-10-717-138-2
Perfect score:     595
Sequence:          1 AYGIGLDITELKRIASMAGR.........SITHTKEYAAAQVVIERLSS 120

Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched:          283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:        283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :         PIR_79:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                                  SUMMARIES
                       %
Result              Query
   No.     Score    Match  Length  DB    ID                        Description
-------------------------------------------------------------------------------
     1       591     99.3     121   1    H69772                    holo-[acyl-carrier
     2       297     49.9     119   2    F83714                    holo-(acyl carrier
     3       287     48.2     118   2    AE1185                    holo-acyl-carrier
     4       283     47.6     118   2    AD1543                    holo-acyl-carrier
     5       275     46.2     119   2    E89999                    holo-ACP synthase
     6       261     43.9     119   2    C86730                    acyl carrier prote
     7       243     40.8     120   2    H95197                    holo-(acyl-carrier
     8       243     40.8     120   2    D98064                    holo-[acyl-carrier
     9     237.5     39.9     126   2    F82072                    holo-(acyl-carrier
    10     221.5     37.2     124   2    B96960                    holo-acyl-carrier
    11     201.5     33.9     169   2    B72345                    holo-(acyl carrier
    12       201     33.8     126   2    F71662                    holo-[acyl-carrier
    13     200.5     33.7     126   2    AF0356                    holo-[acyl-carrier
```

[handwritten annotations: "1999, (1997)" and "(Kunst)" next to result 1; "2000" next to result 2; "2001" next to result 3; "11" next to result 4]

14	195.5	32.9	126	2	E91057	hypothetical prote
15	192.5	32.4	126	2	B85902	hypothetical prote
16	192.5	32.4	126	2	AG0828	holo-[acyl-carrier
17	189.5	31.8	126	1	B42294	holo-[acyl-carrier
18	189	31.8	131	2	A97810	hypothetical prote
19	188.5	31.7	126	2	F84959	holo-[acyl-carrier
20	180.5	30.3	119	2	C71556	holo-[acyl-carrier
21	178.5	30.0	125	2	D81833	holo-[acyl-carrier
22	177.5	29.8	122	2	A86530	acyl-carrier prote
23	177.5	29.8	122	2	B72093	acyl-carrier prote
24	173.5	29.2	125	2	D81710	holo-(acyl-carrier
25	173	29.1	125	2	F71276	holo-[acyl-carrier
26	168.5	28.3	125	2	F81197	holo-(acyl-carrier
27	166.5	28.0	119	1	H64620	holo-[acyl-carrier
28	162.5	27.3	191	2	AC3413	holo-[acyl-carrier
29	161.5	27.1	119	2	G71894	holo-[acyl-carrier
30	158.5	26.6	134	2	H97485	holo-acyl-carrier
31	158.5	26.6	134	2	AH2703	holo-(acyl-carrier
32	151	25.4	123	2	T35573	probable holo-[acy
33	139.5	23.4	133	2	E87442	holo-(acyl-carrier
34	134.5	22.6	122	2	G85649	probable acyl-carr
35	134.5	22.6	122	2	D90789	probable holo-[acy
36	133	22.4	133	2	F75544	probable holo-acyl
37	132.5	22.3	124	2	B70101	holo-acyl-carrier
38	132	22.2	115	2	A81286	probable holo-[acy
39	129.5	21.8	122	2	H70370	holo-[acyl-carrier
40	127.5	21.4	115	2	G82895	holo-acyl carrier
41	124	20.8	1857	1	S01787	fatty-acid synthas
42	115	19.3	130	2	B87058	holo-[acyl-carrier
43	115	19.3	130	2	H70870	holo-[acyl-carrier
44	113	19.0	1885	1	JC4086	fatty-acid synthas
45	104	17.5	119	1	S73864	hypothetical prote

ALIGNMENTS

RESULT 1
H69772
holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: H69772
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo,
V.; Bertero, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Boriss, R.;
Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani,
J.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.;
Duesterhoeft, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi,
A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi,
G.; Guiseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harwood, C.R.; Henaut, A.;
Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.;
Joris, B.; Karamata, D.; Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.;

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OM protein - protein search, using sw model

Run on: May 20, 2005, 02:29:24 ; Search time 14.5075 Seconds
                                          (without alignments)
                                          416.791 Million cell updates/sec

Title: US-10-717-138-1
Perfect score: 397
Sequence: 1 GPLGSADTLERVTKIIVDRL..........EDAEKIATVGDAVNYIQNQQ 81

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

               %
Result   Query
  No.   Score Match Length DB ID   Description
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   1   397   100.0   81   4   US-09-770-834-1   Sequence 1, Appli
   2   238   59.9   79   3   US-09-134-001C-4809   Sequence 4809, Ap
   3   225   56.7   94   4   US-09-543-681A-7956   Sequence 7956, Ap
   4   222.5 56.0   80   4   US-09-902-540-14560   Sequence 14560, A
   5   215   54.2   77   4   US-09-770-834-15   Sequence 15, Appl
   6   215   54.2   108   4   US-09-489-039A-7550   Sequence 7550, Ap
   7   214   53.9   81   4   US-09-252-991A-18646   Sequence 18646, A
   8   205   51.6   372   4   US-09-252-991A-30132   Sequence 30132, A
   9   197   49.6   79   4   US-09-198-452A-308   Sequence 308, App
  10   197   49.6   80   4   US-09-438-185A-297   Sequence 297, App
  11   188   47.4   99   4   US-09-328-352-4669   Sequence 4669, Ap

12	180	45.3	86	4	US-09-107-532A-7143	Sequence 7143, Ap
13	170	42.8	111	4	US-09-248-796A-17438	Sequence 17438, A
14	164.5	41.4	100	4	US-09-902-540-13542	Sequence 13542, A
15	160	40.3	101	4	US-09-107-532A-7092	Sequence 7092, Ap
16	158.5	39.9	74	4	US-09-583-110-3914	Sequence 3914, Ap
17	154	38.8	122	4	US-09-248-796A-17437	Sequence 17437, A
18	153.5	38.7	77	4	US-09-583-110-4176	Sequence 4176, Ap
19	153.5	38.7	84	4	US-09-107-433-4377	Sequence 4377, Ap
20	148.5	37.4	77	3	US-08-858-207A-302	Sequence 302, App
21	134	33.8	97	4	US-09-602-787A-36	Sequence 36, Appl
22	134	33.8	97	4	US-09-852-137-2	Sequence 2, Appli
23	122	30.7	120	3	US-09-056-556-195	Sequence 195, App
24	122	30.7	120	4	US-09-072-596-190	Sequence 190, App
25	122	30.7	120	4	US-09-072-967-195	Sequence 195, App
26	106	26.7	136	2	US-08-580-545B-8	Sequence 8, Appli
27	106	26.7	136	3	US-09-262-653A-8	Sequence 8, Appli
28	99.5	25.1	2756	1	US-08-375-709-11	Sequence 11, Appl
29	99.5	25.1	2756	1	US-08-752-929-11	Sequence 11, Appl
30	99.5	25.1	2756	3	US-09-090-793-7	Sequence 7, Appli
31	99.5	25.1	2756	4	US-09-231-899-7	Sequence 7, Appli
32	97	24.4	41	1	US-08-453-924-8	Sequence 8, Appli
33	94	23.7	110	4	US-09-543-681A-6806	Sequence 6806, Ap
34	93.5	23.6	93	4	US-09-266-965-117	Sequence 117, App
35	91.5	23.0	1481	4	US-09-231-899-70	Sequence 70, Appl
36	85.5	21.5	85	4	US-09-902-540-13340	Sequence 13340, A
37	84	21.2	40	1	US-08-129-129-6	Sequence 6, Appli
38	83	20.9	359	4	US-09-266-965-120	Sequence 120, App
39	76	19.1	84	2	US-08-901-306-4	Sequence 4, Appli
40	75	18.9	90	4	US-09-134-000C-5474	Sequence 5474, Ap
41	74.5	18.8	1610	4	US-09-602-787A-14	Sequence 14, Appl
42	74.5	18.8	1610	4	US-09-602-787A-56	Sequence 56, Appl
43	73	18.4	41	1	US-08-129-129-5	Sequence 5, Appli
44	71.5	18.0	186	4	US-09-248-796A-27171	Sequence 27171, A
45	71	17.9	41	1	US-08-453-924-7	Sequence 7, Appli

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OM protein - protein search, using sw model

Run on: May 20, 2005, 02:31:44 ; Search time 71.3284 Seconds
                                            (without alignments)
                                            379.865 Million cell updates/sec

Title: US-10-717-138-1
Perfect score: 397
Sequence: 1 GPLGSADTLERVTKIIVDRL.........EDAEKIATVGDAVNYIQNQQ 81

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA:*
                 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
                 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
                 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
        %

Result No.	Score	Query Match	Length	DB	ID	Description
1	397	100.0	81	10	US-09-770-834-1	Sequence 1, Appli
2	397	100.0	81	15	US-10-717-138-1	Sequence 1, Appli
3	307	77.3	80	15	US-10-282-122A-46208	Sequence 46208, A
4	284	71.5	77	15	US-10-282-122A-60882	Sequence 60882, A
5	254	64.0	76	9	US-09-815-242-10973	Sequence 10973, A
6	254	64.0	76	15	US-10-282-122A-58089	Sequence 58089, A
7	249	62.7	76	15	US-10-282-122A-67443	Sequence 67443, A
8	239	60.2	110	15	US-10-282-122A-77373	Sequence 77373, A
9	238	59.9	77	15	US-10-282-122A-70919	Sequence 70919, A
10	238	59.9	77	15	US-10-282-122A-71791	Sequence 71791, A
11	236	59.4	77	15	US-10-282-122A-51523	Sequence 51523, A
12	234	58.9	77	9	US-09-815-242-12802	Sequence 12802, A
13	234	58.9	77	9	US-09-815-242-13101	Sequence 13101, A
14	234	58.9	77	15	US-10-282-122A-44414	Sequence 44414, A
15	234	58.9	77	17	US-10-857-625-626	Sequence 626, App
16	232	58.4	73	9	US-09-815-242-5462	Sequence 5462, Ap
17	232	58.4	77	9	US-09-815-242-12124	Sequence 12124, A
18	227	57.2	79	15	US-10-282-122A-51445	Sequence 51445, A
19	226.5	57.1	78	15	US-10-282-122A-78573	Sequence 78573, A
20	225	56.7	104	15	US-10-282-122A-52553	Sequence 52553, A
21	223.5	56.3	75	15	US-10-369-493-8522	Sequence 8522, Ap
22	222.5	56.0	72	15	US-10-369-493-7064	Sequence 7064, Ap
23	222.5	56.0	78	15	US-10-369-493-4308	Sequence 4308, Ap
24	222.5	56.0	79	15	US-10-282-122A-47901	Sequence 47901, A
25	222.5	56.0	79	15	US-10-282-122A-49501	Sequence 49501, A
26	222.5	56.0	79	15	US-10-282-122A-50326	Sequence 50326, A
27	222	55.9	78	15	US-10-369-493-132	Sequence 132, App
28	220	55.4	75	15	US-10-369-493-21035	Sequence 21035, A
29	220	55.4	82	15	US-10-282-122A-61113	Sequence 61113, A
30	217	54.7	71	15	US-10-369-493-9111	Sequence 9111, Ap
31	217	54.7	76	15	US-10-369-493-10628	Sequence 10628, A
32	217	54.7	78	15	US-10-282-122A-65150	Sequence 65150, A
33	216	54.4	78	15	US-10-369-493-12321	Sequence 12321, A
34	216	54.4	78	15	US-10-282-122A-65580	Sequence 65580, A
35	215	54.2	77	10	US-09-770-834-15	Sequence 15, Appl
36	215	54.2	77	15	US-10-717-138-15	Sequence 15, Appl
37	215	54.2	78	9	US-09-815-242-10127	Sequence 10127, A
38	215	54.2	78	14	US-10-230-331-39	Sequence 39, Appl
39	215	54.2	78	15	US-10-369-493-795	Sequence 795, App
40	215	54.2	78	15	US-10-282-122A-43145	Sequence 43145, A
41	215	54.2	78	15	US-10-282-122A-67855	Sequence 67855, A
42	215	54.2	78	15	US-10-282-122A-72742	Sequence 72742, A
43	215	54.2	78	15	US-10-282-122A-75153	Sequence 75153, A
44	215	54.2	78	15	US-10-282-122A-76355	Sequence 76355, A
45	214.5	54.0	75	15	US-10-369-493-18782	Sequence 18782, A

OM protein - protein search, using sw model

Run on: May 20, 2005, 02:27:29 ; Search time 10.0746 Seconds
                                            (without alignments)
                                            773.583 Million cell updates/sec

Title: US-10-717-138-1
Perfect score: 397
Sequence: 1 GPLGSADTLERVTKIIVDRL..........EDAEKIATVGDAVNYIQNQQ 81

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_79:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	370	93.2	77	2	JC4822 Kunst 1997 ✗	acyl carrier prote
2	313	78.8	77	2	B83961	acyl-carrier prote
3	284	71.5	77	2	AF1300	acyl carrier prote
4	284	71.5	77	2	AF1672	acyl carrier prote
5	254	64.0	76	2	C64051	acyl carrier prote
6	244	61.5	77	2	T12052	acyl carrier prote
7	239	60.2	110	2	E82128	acyl carrier prote
8	236	59.4	77	2	F97115	acyl carrier prote
9	234	58.9	77	2	C89896	HmrB protein [impo
10	226.5	57.1	78	2	AC0195	acyl carrier prote
11	222	55.9	78	2	A70448	acyl carrier prote
12	220	55.4	78	2	T44435	acyl carrier prote
13	217.5	54.8	84	2	AG2223	acyl carrier prote

14	216	54.4	78	2	F81222	acyl carrier prote
15	215	54.2	78	1	AYEC	acyl carrier prote
16	215	54.2	78	2	AE0642	acyl carrier prote
17	215	54.2	78	2	D85672	acyl carrier prote
18	215	54.2	78	2	H90812	acyl carrier prote
19	213	53.7	78	2	A83276	acyl carrier prote
20	212	53.4	78	2	T12021	acyl carrier prote
21	212	53.4	78	2	A36728	acyl carrier prote
22	211	53.1	77	2	H71541	probable acyl carr
23	209	52.6	78	2	AG2711	acyl carrier prote
24	209	52.6	78	2	AE3436	acyl carrier prote
25	204	51.4	78	2	C87457	acyl carrier prote
26	203	51.1	77	2	D81695	acyl carrier prote
27	203	51.1	77	2	S77465	acyl carrier prote
28	202	50.9	110	2	F75333	acyl carrier prote
29	201	50.6	78	2	H71922	acyl carrier prote
30	200.5	50.5	79	2	D83411	probable acyl carr
31	200	50.4	77	2	G81388	acyl carrier prote
32	200	50.4	80	2	H84970	acyl carrier prote
33	197	49.6	79	2	G86527	acyl carrier prote
34	197	49.6	79	2	C72096	acyl carrier prote
35	196	49.4	81	2	C72349	acyl carrier prote
36	194	48.9	78	2	G64589	acyl carrier prote
37	193	48.6	80	2	S78295	acyl carrier prote
38	192.5	48.5	76	2	S13819	acyl carrier prote
39	192	48.4	80	2	A39452	acyl carrier prote
40	189	47.6	123	2	C71616	acyl carrier prote
41	188	47.4	85	2	G82776	ACP XF0672 [import
42	187	47.1	84	2	S73201	acyl carrier prote
43	184.5	46.5	153	2	B64640	acyl carrier prote
44	184	46.3	69	2	B36728	acyl carrier prote
45	176	44.3	80	2	C41609	acyl carrier prote

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OM protein - protein search, using sw model

Run on: May 20, 2005, 02:26:43 ; Search time 91.4776 Seconds
                                         (without alignments)
                                         453.427 Million cell updates/sec

Title: US-10-717-138-1
Perfect score: 397
Sequence: 1 GPLGSADTLERVTKIIVDRL.........EDAEKIATVGDAVNYIQNQQ 81

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_03:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                 SUMMARIES
                    %
Result   Query
  No.   Score   Match Length DB   ID   ·Description
----
 1   370   93.2   77   1   ACP_BACSU /996 X   P80643 bacillus su
 2   345   86.9   77   2   Q65JQ6   Q65jq6 bacillus li
 3   313   78.8   77   1   ACP_BACHD   Q9ka04 bacillus ha
 4   302   76.1   77   1   ACP_BACAN   Q81wi7 bacillus an
 5   302   76.1   77   1   ACP_BACCR   Q819v7 bacillus ce
 6   302   76.1   77   2   Q636H6   Q636h6 bacillus ce
 7   302   76.1   77   2   Q732M0   Q732m0 bacillus ce
 8   302   76.1   77   2   Q6HEW5   Q6hew5 bacillus th
 9   284   71.5   77   1   ACP_LISIN   P63440 listeria in
 10   284   71.5   77   1   ACP_LISMO   P63439 listeria mo
 11   284   71.5   77   2   Q71YL0   Q71yl0 listeria mo
 12   271   68.3   77   1   ACP_OCEIH   Q8er06 oceanobacil
 13   254   64.0   76   1   ACP_HAEIN   P43709 haemophilus
 14   254   64.0   76   2   Q65RC8   Q65rc8 mannheimia
 15   249   62.7   76   1   ACP_PASMU   Q9cjs5 pasteurella

16	249	62.7	83	2	Q67PF6	Q67pf6 symbiobacte
17	244	61.5	76	1	ACP_VIBPA	P55337 vibrio para
18	239	60.2	77	1	ACP_VIBCH	Q9kqh8 vibrio chol
19	238	59.9	77	1	ACP_STAEP	Q8cpi2 staphylococ
20	236	59.4	77	1	ACP_CLOAB	Q97ia5 clostridium
21	236	59.4	77	1	ACP_VIBVU	Q8d8g9 vibrio vuln
22	236	59.4	78	2	Q7MLZ9	Q7mlz9 vibrio vuln
23	235	59.2	77	1	ACP_HAEDU	Q7vkh6 haemophilus
24	234	58.9	77	1	ACP_STAAM	Q99qn7 staphylococ
25	234	58.9	77	2	Q6G9Y1	Q6g9y1 staphylococ
26	234	58.9	77	2	Q6GHK3	Q6ghk3 staphylococ
27	233	58.7	76	1	ACP_THETN	Q8r9w1 thermoanaer
28	233	58.7	78	2	Q7N387	Q7n387 photorhabdu
29	232	58.4	78	1	ACP_PHOPR	Q9r6z3 photobacter
30	230	57.9	77	1	ACP_SHEON	Q8edh4 shewanella
31	230	57.9	77	2	Q74CR8	Q74cr8 geobacter s
32	230	57.9	77	2	Q75FW6	Q75fw6 leptospira
33	230	57.9	77	2	Q8EXX4	Q8exx4 leptospira
34	228	57.4	98	2	Q7W5I7	Q7w5i7 bordetella
35	228	57.4	103	2	Q7NI72	Q7ni72 gloeobacter
36	227	57.2	79	2	Q7VW32	Q7vw32 bordetella
37	227	57.2	79	2	Q7WD23	Q7wd23 bordetella
38	226.5	57.1	77	1	ACP_YERPE	Q8zft4 yersinia pe
39	226.5	57.1	78	2	Q669L4	Q66914 yersinia ps
40	224	56.4	76	2	Q72CS8	Q72cs8 desulfovibr
41	223.5	56.3	79	1	ACP1_RALSO	Q8y0j1 ralstonia s
42	223	56.2	78	2	Q8A2E6	Q8a2e6 bacteroides
43	222.5	56.0	79	2	Q62LT9	Q62lt9 burkholderi
44	222.5	56.0	79	2	Q63S86	Q63s86 burkholderi
45	222	55.9	78	1	ACP_AQUAE	O67611 aquifex aeo

ALIGNMENTS

RESULT 1
ACP_BACSU
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ID   ACP_BACSU       STANDARD;       PRT;      77 AA.
AC   P80643; P51832;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Acyl carrier protein (ACP).
GN   Name=acpA; Synonyms=acpP; OrderedLocusNames=BSU15920;
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE OF 15-77, AND SEQUENCE OF 1-14 FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=96326321; PubMed=8759840;
RA   Morbidoni H.R., de Mendoza D., Cronan J.E. Jr.;
RT   "Bacillus subtilis acyl carrier protein is encoded in a cluster of
RT   lipid biosynthesis genes.";
RL   J. Bacteriol. 178:4794-4800(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
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                          GenCore version 5.1.6
                Copyright (c) 1993 - 2005  Compugen Ltd.


OM protein - protein search, using sw model

Run on:          May 20, 2005, 02:25:38 ; Search time 53.194 Seconds
                                          (without alignments)
                                          588.931 Million cell updates/sec

Title:           US-10-717-138-1
Perfect score:   397
Sequence:        1 GPLGSADTLERVTKIIVDRL.........EDAEKIATVGDAVNYIQNQQ 81

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:        2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_16Dec04:*
                 1:  geneseqp1980s:*
                 2:  geneseqp1990s:*
                 3:  geneseqp2000s:*
                 4:  geneseqp2001s:*
                 5:  geneseqp2002s:*
                 6:  geneseqp2003as:*
                 7:  geneseqp2003bs:*
                 8:  geneseqp2004s:*


      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.


                             SUMMARIES
                   %
Result          Query
  No.    Score   Match Length DB  ID                          Description
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    1     397    100.0     81  5  AAU10693  2002 Appl WO   Aau10693 B. subtil   not subhlr
    2     307     77.3     80  6  ABU18284  o3            Abu18284 Protein e
    3     284     71.5     77  5  ABB49632                Abb49632 Listeria
    4     284     71.5     77  6  ABU32958                Abu32958 Protein e
    5     254     64.0     76  4  AAU35380                Aau35380 Haemophil
    6     254     64.0     76  6  ABU30165                Abu30165 Protein e
    7     249     62.7     76  6  ABU39519                Abu39519 Protein e
    8     239     60.2    110  6  ABU49449                Abu49449 Protein e
    9     238     59.9     77  6  ABU43867                Abu43867 Protein e
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10	238	59.9	77	6	ABU42995	Abu42995	Protein e
11	238	59.9	79	5	ABP39964	Abp39964	Staphyloc
12	238	59.9	79	8	ADS06306	Ads06306	Staphyloc
13	236	59.4	77	6	ABU23599	Abu23599	Protein e
14	234	58.9	77	4	AAU37508	Aau37508	Staphyloc
15	234	58.9	77	4	AAU37209	Aau37209	Staphyloc
16	234	58.9	77	4	AAE02204	Aae02204	Staphyloc
17	234	58.9	77	6	ABU16490	Abu16490	Protein e
18	234	58.9	77	6	ABM73195	Abm73195	Staphyloc
19	232	58.4	73	4	AAU33966	Aau33966	Staphyloc
20	232	58.4	77	4	AAU36531	Aau36531	Staphyloc
21	227	57.2	79	6	ABU23521	Abu23521	Protein e
22	226.5	57.1	78	6	ABU50649	Abu50649	Protein e
23	225	56.7	94	7	ADF07671	Adf07671	Bacterial
24	225	56.7	104	6	ABU24629	Abu24629	Protein e
25	223.5	56.3	48	5	AAM47181	Aam47181	Modular e
26	223.5	56.3	75	8	ADN25869	Adn25869	Bacterial
27	222.5	56.0	72	8	ADN24411	Adn24411	Bacterial
28	222.5	56.0	78	8	ADN21655	Adn21655	Bacterial
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30	222.5	56.0	79	6	ABU22402	Abu22402	Protein e
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33	222	55.9	80	6	ADB10328	Adb10328	Alloiococ
34	220	55.4	75	8	ADS42605	Ads42605	Bacterial
35	220	55.4	82	6	ABU33189	Abu33189	Protein e
36	217	54.7	71	8	ADN26458	Adn26458	Bacterial
37	217	54.7	76	8	ADS21595	Ads21595	Bacterial
38	217	54.7	78	6	ABP80257	Abp80257	N. gonorr
39	217	54.7	78	6	ABP78733	Abp78733	N. gonorr
40	217	54.7	78	6	ABU37226	Abu37226	Protein e
41	217	54.7	90	6	ABP78743	Abp78743	N. gonorr
42	216	54.4	78	6	ABU37656	Abu37656	Protein e
43	216	54.4	78	8	ADS23288	Ads23288	Bacterial
44	215	54.2	78	4	AAU34534	Aau34534	E. coli c
45	215	54.2	78	4	AAE02208	Aae02208	Escherich

RESULT 1 (SEQ ID NO. 1)

ACP_BACSU

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ID   ACP_BACSU      STANDARD;      PRT;     77 AA.
AC   P80643; P51832;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
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OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE OF 15-77, AND SEQUENCE OF 1-14 FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=96326321; PubMed=8759840;
RA   Morbidoni H.R., de Mendoza D., Cronan J.E. Jr.;
RT   "Bacillus subtilis acyl carrier protein is encoded in a cluster of
RT   lipid biosynthesis genes.";
RL   J. Bacteriol. 178:4794-4800(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=96257247; PubMed=8654983; DOI=10.1016/0378-1119(96)00181-3;
RA   Oguro A., Kakeshita H., Takamatsu H., Nakamura K., Yamane K.;
RT   "The effect of Srb, a homologue of the mammalian SRP receptor alpha-
RT   subunit, on Bacillus subtilis growth and protein translocation.";
RL   Gene 172:17-24(1996).
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RC   STRAIN=168;
RX   MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA   Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA   Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA   Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA   Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA   Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA   Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA   Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA   Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA   Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA   Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
RA   Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA   Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
RA   Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA   Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA   Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA   Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA   Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA   Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA   Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA   Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA   Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
RA   Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
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RA   Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA   Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA   Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA   Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA   Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
RA   Yoshikawa H., Danchin A.;
RT   "The complete genome sequence of the Gram-positive bacterium Bacillus
RT   subtilis.";
RL   Nature 390:249-256(1997).
RN   [4]
RP   SEQUENCE OF 1-17.
RX   MEDLINE=94131947; PubMed=8300523;
RA   Heaton M.P., Neuhaus F.C.;
RT   "Role of the D-alanyl carrier protein in the biosynthesis of D-alanyl-
RT   lipoteichoic acid.";
RL   J. Bacteriol. 176:681-690(1994).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF HOLO-(ACYL CARRIER PROTEIN)
RP   IN COMPLEX WITH HOLO-(ACYL CARRIER PROTEIN) SYNTHASE.
RX   PubMed=10997907; DOI=10.1016/S0969-2126(00)00178-7;
RA   Parris K.D., Lin L., Tam A., Mathew R., Hixon J., Stahl M.,
RA   Fritz C.C., Seehra J., Somers W.S.;
RT   "Crystal structures of substrate binding to Bacillus subtilis holo-
RT   (acyl carrier protein) synthase reveal a novel trimeric arrangement of
RT   molecules resulting in three active sites.";
RL   Structure 8:883-895(2000).
RN   [6]
RP   STRUCTURE BY NMR.
RX   MEDLINE=21416009; PubMed=11525165; DOI=10.1016/S0969-2126(01)00586-X;
RA   Xu G.Y., Tam A., Lin L., Hixon J., Fritz C.C., Powers R.;
RT   "Solution structure of B. subtilis acyl carrier protein.";
RL   Structure 9:277-287(2001).
CC   -!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC   biosynthesis.
CC   -!- PATHWAY: De novo fatty acid biosynthesis.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC   serine of apo-ACP by acpS. This modification is essential for
CC   activity because fatty acids are bound in thioester linkage to the
CC   sulfhydryl of the prosthetic group.
CC   -!- SIMILARITY: Contains 1 acyl carrier domain.
CC   --
DR   EMBL; U59433; AAC44308.1; -.
DR   EMBL; D64116; BAA10975.1; -.
DR   EMBL; Z99112; CAB13465.1; -.
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DR   PIR; T46634; T46634.
DR   PDB; 1F80; X-ray; D/E/F=1-77.
DR   PDB; 1HY8; NMR; A=2-77.

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DR     InterPro; IPR003231; Acyl_carrier.
DR     InterPro; IPR006163; Pp_bind.
DR     InterPro; IPR006162; Ppantne_S.
DR     Pfam; PF00550; PP-binding; 1.
DR     ProDom; PD000887; Acyl_carrier; 1.
DR     TIGRFAMs; TIGR00517; acyl_carrier; 1.
DR     PROSITE; PS50075; ACP_DOMAIN; 1.
DR     PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
KW     3D-structure; Complete proteome; Direct protein sequencing;
KW     Fatty acid biosynthesis; Lipid synthesis; Phosphopantetheine.
FT     BINDING        37       37           Phosphopantetheine.
FT     HELIX           3       16
FT     TURN           25       26
FT     STRAND         28       28
FT     HELIX          29       33
FT     HELIX          37       50
FT     TURN           51       52
FT     HELIX          57       61
FT     TURN           62       62
FT     STRAND         65       65
FT     HELIX          66       74
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H69772

(SEQ ID NO: 2)

holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: H69772
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo,
V.; Bertero, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Boriss, R.;
Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani,
J.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.;
Duesterhoeft, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi,
A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi,
G.; Guiseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harwood, C.R.; Henaut, A.;
Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.;
Joris, B.; Karamata, D.; Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.;
Kobayashi, Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.;
Lapidus, A.; Lardinois, S.
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda,
S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.;
Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Oudega,
B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott,
A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds,
S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato,
T.; Scanlon, E.
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska,
A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.;
Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka,
T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, M.; Vannier,
F.; Vassarotti, A.; Viari, A.; Wambutt, R.; Wedler, E.; Wedler, H.;
Weitzenegger, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto,
K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: H69772
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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A;Cross-references: UNIPROT:P96618; GB:Z99106; GB:AL009126; NID:g2632653;
PIDN:CAB12269.1; PID:g2632762
A;Experimental source: strain 168
C;Genetics:
A;Gene: ydcB
C;Superfamily: holo-ACP synthase
C;Keywords: coenzyme A; transferase

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Query Match               99.3%;  Score 591;  DB 1;  Length 121;
Best Local Similarity     100.0%;  Pred. No. 1.1e-51;
Matches  119;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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